

BLASTP 2.2.9 [May-01-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1084307128-16635-68711394475.BLASTQ3

Query=

(191 letters) SEQ ID NO: 206

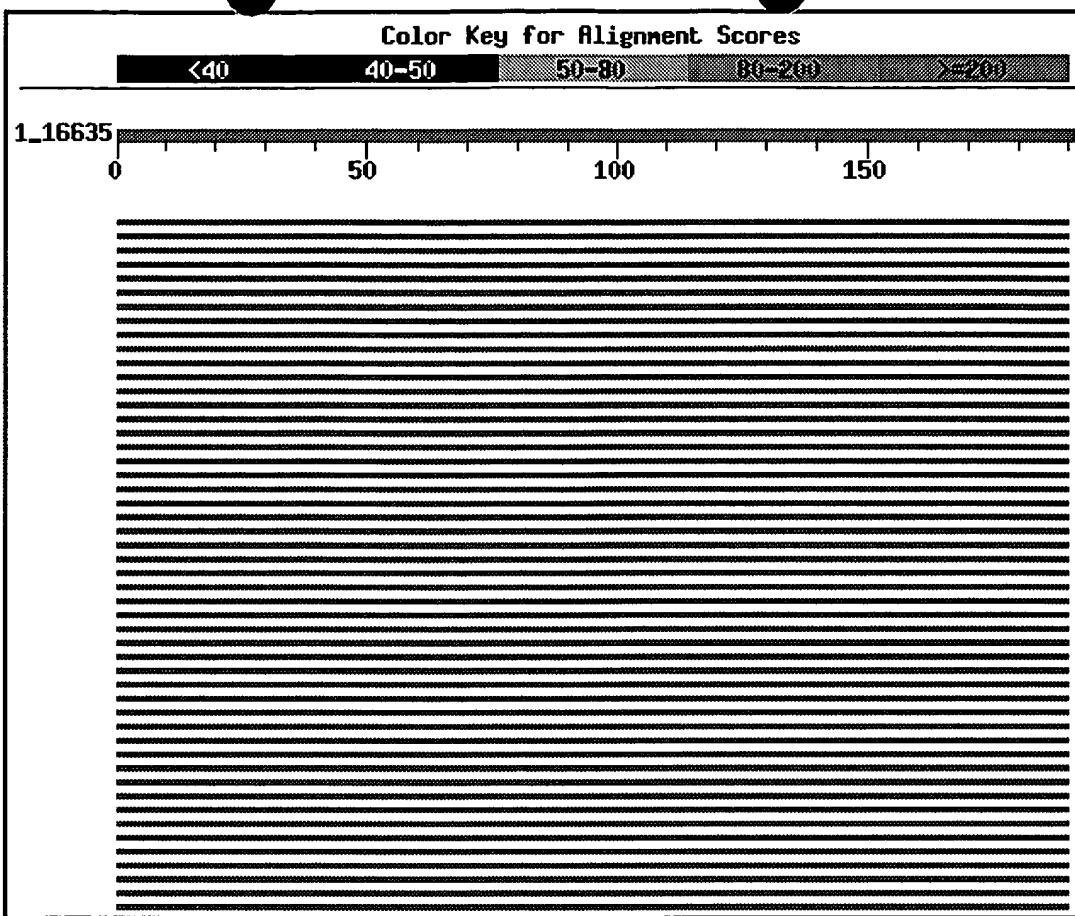
Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples
1,798,171 sequences; 593,787,773 total letters

If you have any problems or questions with the results of this search
please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



		Score	E	Value
Sequences producing significant alignments:		(bits)		
gi 2326455 emb CAA72801.1	polyprotein [Hepatitis C virus t...	<u>293</u>	2e-78	
gi 3550763 dbj BAA32666.1	polyprotein [Hepatitis C virus]	<u>291</u>	4e-78	
gi 3550761 dbj BAA32665.1	polyprotein [Hepatitis C virus]	<u>285</u>	5e-76	
gi 3550765 dbj BAA32667.1	polyprotein [Hepatitis C virus]	<u>285</u>	5e-76	
gi 600265 dbj BAA13617.1	core, env and part of E2/NS1 [Hep...	<u>282</u>	2e-75	
gi 1765877 dbj BAA13620.1	core, env and part of E2/NS1 [He...	<u>282</u>	3e-75	
gi 1765873 dbj BAA13618.1	core, env and part of E2/NS1 [He...	<u>281</u>	5e-75	
gi 1765875 dbj BAA13619.1	core, env and part of E2/NS1 [He...	<u>280</u>	8e-75	
gi 2252490 emb CAA72338.1	HCV polyprotein [Hepatitis C vir...	<u>280</u>	9e-75	
gi 3550759 dbj BAA32664.1	polyprotein [Hepatitis C virus]	<u>280</u>	1e-74	
gi 1765881 dbj BAA13622.1	core, env and part of E2/NS1 [He...	<u>280</u>	1e-74	
gi 7650248 gb AAF65955.1	polyprotein [Hepatitis C virus]	<u>280</u>	1e-74	
gi 464178 dbj BAA03581.1	polyprotein [Hepatitis C virus]	<u>279</u>	2e-74	
gi 1765885 dbj BAA13624.1	core, env and part of E2/NS1 [He...	<u>279</u>	2e-74	
gi 1765879 dbj BAA13621.1	core, env and part of E2/NS1 [He...	<u>279</u>	2e-74	
gi 1765887 dbj BAA13625.1	core, env and part of E2/NS1 [He...	<u>279</u>	3e-74	
gi 7650256 gb AAF65959.1	polyprotein [Hepatitis C virus]	<u>278</u>	3e-74	
gi 482138 pir S40770	genome polyprotein - hepatitis C viru...	<u>278</u>	4e-74	
gi 2327073 gb AAB67037.1	polyprotein [Hepatitis C virus st...	<u>278</u>	4e-74	
gi 471117 dbj BAA01728.1	polyprotein precursor [Hepatitis ...	<u>278</u>	4e-74	
gi 130461 sp P27958 POLG_HCVH	Genome polyprotein [Contains:...]	<u>278</u>	4e-74	
gi 8926245 gb AAF81759.1	polyprotein [Hepatitis C virus]	<u>278</u>	4e-74	
gi 130455 sp P26664 POLG_HCV1	Genome polyprotein [Contains:...]	<u>278</u>	4e-74	

gi 14532245 gb AAK66554.1	HCV type 1a/1b chimera polyprote...	278	5e-74
gi 2327071 gb AAB67036.1	polyprotein [Hepatitis C virus st...	278	5e-74
gi 22129793 ref NP_671491.1	polyprotein [Hepatitis C virus...	278	5e-74
gi 14532251 gb AAK66557.1	HCV type 1a/1b chimera mutant po...	278	5e-74
gi 2327075 gb AAB67038.1	polyprotein [Hepatitis C virus st...	278	5e-74
gi 9930557 gb AAG02099.1	polyprotein [Hepatitis C virus]	278	5e-74
gi 3098655 gb AAC15732.1	polyprotein [Hepatitis C virus]	277	6e-74
gi 15529111 gb AAK97744.1	polyprotein [Hepatitis C virus]	277	6e-74
gi 1944376 dbj BAA19625.1	unnamed protein product [Hepatit...	277	7e-74
gi 1009261 dbj BAA07091.1	core, env and part of E2/NS1 [He...	277	7e-74
gi 3098644 gb AAC15727.1	polyprotein [Hepatitis C virus]	277	7e-74
gi 5918961 gb AAD56196.1	polyprotein [Hepatitis C virus]	277	8e-74
gi 2943784 dbj BAA25076.1	polyprotein [Hepatitis C virus]	277	8e-74
gi 7650246 gb AAF65954.1	polyprotein [Hepatitis C virus]	277	8e-74
gi 7650240 gb AAF65951.1	polyprotein [Hepatitis C virus]	277	9e-74
gi 5420377 emb CAB46677.1	polyprotein [Hepatitis C virus t...	277	9e-74
gi 5918963 gb AAD56197.1	polyprotein [Hepatitis C virus]	277	9e-74
gi 7650244 gb AAF65953.1	polyprotein [Hepatitis C virus]	277	9e-74
gi 7650224 gb AAF65943.1	polyprotein [Hepatitis C virus]	277	1e-73
gi 7650234 gb AAF65948.1	polyprotein [Hepatitis C virus]	277	1e-73
gi 7341103 gb AAF61205.1	polyprotein [Hepatitis C virus]	276	1e-73
gi 1814086 dbj BAA09072.1	polyprotein [Hepatitis C virus]	276	1e-73
gi 7650252 gb AAF65957.1	polyprotein [Hepatitis C virus]	276	1e-73
gi 1814089 dbj BAA09076.1	polyprotein [Hepatitis C virus]	276	1e-73
gi 1765868 dbj BAA13615.1	core, env and part of E2/NS1 [He...	276	1e-73
gi 1009263 dbj BAA07092.1	core, env and part of E2/NS1 [He...	276	1e-73
gi 7650226 gb AAF65944.1	polyprotein [Hepatitis C virus]	276	2e-73
gi 221607 dbj BAA01583.1	polyprotein precursor [Hepatitis ...	276	2e-73
gi 1009271 dbj BAA07271.1	core, env and part of E2/NS1 [He...	276	2e-73
gi 1765870 dbj BAA13616.1	core, env, and part of E2/NS1 [He...	275	2e-73
gi 1009257 dbj BAA07089.1	core, env, and part of E2/NS1 [He...	275	3e-73
gi 1009259 dbj BAA07090.1	core, env and part of E2/NS1 [He...	275	3e-73
gi 1765866 dbj BAA13614.1	core, env and part of E2/NS1 [He...	274	5e-73
gi 3523057 dbj BAA32652.1	polyprotein [Hepatitis C virus]	274	5e-73
gi 3523059 dbj BAA32653.1	polyprotein [Hepatitis C virus]	274	6e-73
gi 1009265 dbj BAA07093.1	core, env and part of E2/NS1 [He...	273	9e-73
gi 3523055 dbj BAA32651.1	polyprotein [Hepatitis C virus]	273	1e-72
gi 1066618 gb AAC42193.1	core protein	273	1e-72
gi 1765891 dbj BAA13627.1	core, env and part of E2/NS1 [He...	273	1e-72
gi 601937 dbj BAA06739.1	core, env and part of E2/NS1 [Hep...	272	2e-72
gi 1765883 dbj BAA13623.1	core, env and part of E2/NS1 [He...	272	2e-72
gi 540813 pir PN0677	hypothetical protein 787 - hepatitis ...	271	6e-72
gi 1765889 dbj BAA13626.1	core, env and part of E2/NS1 [He...	270	1e-71
gi 1009269 dbj BAA07095.1	core, env and part of E2/NS1 [He...	270	1e-71
gi 1372958 gb AAB02127.1	polyprotein [Hepatitis C virus]	270	2e-71
gi 2580421 dbj BAA23132.1	polyprotein [Hepatitis C virus]	269	2e-71
gi 410168 gb AAA20154.1	structural region	269	3e-71
gi 1009255 dbj BAA07088.1	polyprotein [Hepatitis C virus]	268	3e-71
gi 22212866 gb AAM94419.1	polyprotein [Hepatitis C virus]	268	4e-71
gi 37961928 gb AAP69953.1	polyprotein [Hepatitis C virus]	268	4e-71
gi 93949 pir S12707	genome polyprotein - hepatitis C virus...	268	6e-71
gi 1009267 dbj BAA07094.1	core, env, and part of E2/NS1 [He...	268	6e-71
gi 13344959 gb AAK19133.1	polyprotein precursor [Hepatitis...	266	2e-70
gi 1066620 gb AAC42194.1	core protein	266	2e-70
gi 13344949 gb AAK19128.1	polyprotein precursor [Hepatitis...	265	3e-70
gi 23328866 gb AAC42195.2	core protein [Hepatitis C virus]	265	4e-70
gi 474978 dbj BAA03730.1	polyprotein [Hepatitis C virus]	265	4e-70
gi 1181855 gb AAA86917.1	polyprotein	265	4e-70
gi 13344947 gb AAK19127.1	polyprotein precursor [Hepatitis...	265	4e-70
gi 464172 dbj BAA03732.1	polyprotein [Hepatitis C virus]	265	5e-70

<u>gi 13344953 gb AAK19130.1 </u>	polyprotein precursor [Hepatitis...	<u>264</u>	6e-70
<u>gi 13344951 gb AAK19129.1 </u>	polyprotein precursor [Hepatitis...	<u>264</u>	6e-70
<u>gi 13344963 gb AAK19135.1 </u>	polyprotein precursor [Hepatitis...	<u>263</u>	9e-70
<u>gi 13344969 gb AAK19138.1 </u>	polyprotein precursor [Hepatitis...	<u>263</u>	1e-69
<u>gi 13344961 gb AAK19134.1 </u>	polyprotein precursor [Hepatitis...	<u>263</u>	1e-69
<u>gi 13344967 gb AAK19137.1 </u>	polyprotein precursor [Hepatitis...	<u>263</u>	1e-69
<u>gi 13344965 gb AAK19136.1 </u>	polyprotein precursor [Hepatitis...	<u>263</u>	1e-69
<u>gi 221512 dbj BAA00705.1 </u>	structural protein [Hepatitis C v...	<u>263</u>	1e-69
<u>gi 1066604 gb AAC42186.1 </u>	core protein	<u>263</u>	2e-69
<u>gi 532381 gb AAA21037.1 </u>	polyprotein	<u>263</u>	2e-69
<u>gi 913996 gb AAB34375.1 </u>	polyprotein [Hepatitis C virus]	<u>262</u>	3e-69
<u>gi 974347 gb AAB40038.1 </u>	core protein [Hepatitis C virus ty...	<u>260</u>	9e-69
<u>gi 1066606 gb AAC42187.1 </u>	core protein	<u>260</u>	1e-68
<u>gi 329736 gb AAA98989.1 </u>	capsid and envelope:x proteins	<u>259</u>	2e-68
<u>gi 1369771 gb AAB02117.1 </u>	core protein	<u>259</u>	2e-68
<u>gi 38147542 gb AAR12079.1 </u>	polyprotein [Hepatitis C virus]	<u>258</u>	4e-68
<u>gi 1246371 dbj BAA09974.1 </u>	polyprotein [Hepatitis C virus]	<u>251</u>	4e-66

Alignments

<input type="checkbox"/> <u>gi 2326455 emb CAA72801.1 </u>	polyprotein [Hepatitis C virus type 6a]
	Length = 3018
	Score = 293 bits (749), Expect = 2e-78
	Identities = 144/191 (75%), Positives = 145/191 (75%)
Query: 1	MSTLPKPQXXXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
	MSTLPKPQ P DVKFPGGGQIV ATRKTTSERSQPRG
Sbjct: 1	MSTLPKPQRKTKRNTNRRPMVDVKFPGGGQIVGGVYLLPRKGPRLGVRATRKTTSERSQPRG 60
Query: 61	RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
	RRQPIPKARQPQGRHWAQPGYPWPLYG+EGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG
Sbjct: 61	RRQPIPKARQPQGRHWAQPGYPWPLYGSEGC GWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
Query: 121	KVIDTLCGFADLMGYXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
	KVIDTLCGFADLM YI RAIEDGINYATGNLPGCSFSIFLLA
Sbjct: 121	KVIDTLCGFADLMWYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180
Query: 181	LLSCLTTTPASA 191
	LLSCLTTTPASA
Sbjct: 181	LLSCLTTTPASA 191
<input type="checkbox"/> <u>gi 3550763 dbj BAA32666.1 </u>	polyprotein [Hepatitis C virus]
	Length = 3016
	Score = 291 bits (745), Expect = 4e-78
	Identities = 144/191 (75%), Positives = 145/191 (75%)
Query: 1	MSTLPKPQXXXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
	MSTLPKPQ P DVKFPGGGQIV ATRKTTSERSQPRG
Sbjct: 1	MSTLPKPQRKTKRNTNRRPMVDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
RRQPIPKARQ QGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRP+WGPNDPRRRSRN LG
Sbjct: 61 RRQPIPKARQSQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPNWGPNDPRRRSRN LG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI RAIEDGINYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTTPASA 191
LLSCLTTTPASA
Sbjct: 181 LLSCLTTTPASA 191

>gi|3550761|dbj|BAA32665.1| polyprotein [Hepatitis C virus]
Length = 3013

Score = 285 bits (728), Expect = 5e-76
Identities = 140/191 (73%), Positives = 142/191 (74%)

Query: 1 MSTLPKPQXXXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MSTLPKPQ P DVKFPGGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTLPKPQKRNQRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
RRQPIPKAR+ GR WAQPGYPWPLYGNEGCGW GWLLSPRGSRPHWGPNDPRRRSRN LG
Sbjct: 61 RRQPIPKARRQTGRTWAQPGYPWPLYGNEGCGWMGWLLSPRGSRPHWGPNDPRRRSRN LG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI RA+EDGINYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLMGYIPVVGAPLGGVAAALAHGVRAVEDGINYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTTPASA 191
LLSCLTTTPASA
Sbjct: 181 LLSCLTTTPASA 191

>gi|3550765|dbj|BAA32667.1| polyprotein [Hepatitis C virus]
Length = 3015

Score = 285 bits (728), Expect = 5e-76
Identities = 140/191 (73%), Positives = 142/191 (74%)

Query: 1 MSTLPKPQXXXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MSTLPKPQ P DVKFPGGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTLPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
RRQPIPKARQP GR W QPGYPWPLYGNEGCGWAGWLLSPRGSRP+WGPNDPRRRSRN LG
Sbjct: 61 RRQPIPKARQPIGRSGWQPGYPWPLYGNEGCGWAGWLLSPRGSRPNWGPNDPRRRSRN LG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCG ADLMGYI RAIEDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGLADLMGYIPVLLGGPLGGVAAALAHGVRAIEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTTPASA 191
LLSCLTTTPASA
Sbjct: 181 LLSCLTTTPASA 191

>gi|600265|dbj|BAA13617.1| core, env and part of E2/NS1 [Hepatitis C virus]
Length = 414

Score = 282 bits (722), Expect = 2e-75
Identities = 144/191 (75%), Positives = 145/191 (75%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MSTLPKPQ P DVKFPGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTLPKPQRKTKRNTNRRPMVDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60
Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRSRNLG 120
RRQPIPKARQ P GRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRP+WGPNPDRRSRNLG
Sbjct: 61 RRQPIPKARQSQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPNWGPNDPDRRSRNLG 120
Query: 121 KVIDTLCGFADLIMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLIMGYI RAIEDGINYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLIMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180
Query: 181 LLSCLTTTPASA 191
LLSCLTTTPASA
Sbjct: 181 LLSCLTTTPASA 191

>gi|1765877|dbj|BAA13620.1| core, env and part of E2/NS1 [Hepatitis C virus]
Length = 414

Score = 282 bits (721), Expect = 3e-75
Identities = 143/191 (74%), Positives = 144/191 (75%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MSTLPKPQ P DVKFPGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTLPKPQRKTKRNTNRRPMVDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60
Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRSRNLG 120
RRQPIPKARQ P GRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPDRRSRNLG
Sbjct: 61 RRQPIPKARQPTGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPDRRSRNLG 120
Query: 121 KVIDTLCGFADLIMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDT+TCGFADLIMGYI R IEDGINYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTITCGFADLIMGYIPVLGAPLGGVAAALAHGVRVIEDGINYATGNLPGCSFSIFLLA 180
Query: 181 LLSCLTTTPASA 191
LLSCLTTTPASA
Sbjct: 181 LLSCLTTTPASA 191

>gi|1765873|dbj|BAA13618.1| core, env and part of E2/NS1 [Hepatitis C virus]
Length = 414

Score = 281 bits (719), Expect = 5e-75
Identities = 143/191 (74%), Positives = 144/191 (75%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MSTLPKPQ P DVKFPGGQIV ATRKTTSERSQPRG

Sbjct: 1 MSTLPKPQRKTKRNTNRRPMDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRG 60
Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
RRQPIPKARQ QGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG
Sbjct: 61 RRQPIPKARQSQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI RA+EDGINYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLMGYIPVVGAPLGGVAAALAHGVRALEDGINYATGNLPGCSFSIFLLA 180
Query: 181 LLSCLTTPASA 191
LLSCLTTP SA
Sbjct: 181 LLSCLTTPASA 191

>gi|1765875|dbj|BAA13619.1| core, env and part of E2/NS1 [Hepatitis C virus]
Length = 414

Score = 280 bits (717), Expect = 8e-75
Identities = 142/191 (74%), Positives = 143/191 (74%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGQIVXXXXXXXXXXXXATRKTSESRQPRG 60
MSTLPKPQ P DVKFPGGQIV ATRKTSESRQPRG
Sbjct: 1 MSTLPKPQRKTKRNTNRRPMDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRG 60
Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
RRQPIPKARQP GRHWAQPGY WPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG
Sbjct: 61 RRQPIPKARQPTGRHWAQPGYAWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDT+TCGFADLMGYI R IEDGINYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTITCGFADLMGYIPVLGAPLGGVAAALAHGVVIEDGINYATGNLPGCSFSIFLLA 180
Query: 181 LLSCLTTPASA 191
LLSCLTTPASA
Sbjct: 181 LLSCLTTPASA 191

>gi|2252490|emb|CAA72338.1| HCV polyprotein [Hepatitis C virus type 4a]
Length = 3008

Score = 280 bits (717), Expect = 9e-75
Identities = 138/191 (72%), Positives = 141/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGQIVXXXXXXXXXXXXATRKTSESRQPRG 60
MST PKPQ P DVKFPGGQIV ATRKTSESRQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPMDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRG 60
Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
RRQPIPKAR+P+GR WAQPGY WPLYGNEGCGWAGWLLSPRGSRPHWGPNDP RSRNLG
Sbjct: 61 RRQPIPKARRPEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRGRSRNLG 120
Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI RA+EDGINYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLMGYIPVLGAPVGSVARALAHGVRALEDGINYATGNLPGCSFSIFLLA 180
Query: 181 LLSCLTTPASA 191

LLSCLT PASA
Sbjct: 181 LLSCLTVPASA 191

□ >gi|3550759|dbj|BAA32664.1| polyprotein [Hepatitis C virus]
Length = 3019

Score = 280 bits (716), Expect = 1e-74
Identities = 138/191 (72%), Positives = 140/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MSTLPKPQ P DVKFPGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTLPKPQRKTKRNTNRRPMDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNECGWAGWLSPRGSRPHGPNDPRRRSRN LG 120
RRQPIPKAR QGR W QPGYPWPLYGNECGWAGWL+SPRGSRP WGPNDPRRRSRN LG
Sbjct: 61 RRQPIPKARPSQGRTWGQPGYPWPLYGNECGWAGWLSPRGSRPSWGPNDPRRRSRN LG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCG ADLMGYI RAIEDGINYATGNLPGCSFSIF+LA
Sbjct: 121 KVIDTLCGLADLMGYIPVVGGLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFILA 180

Query: 181 LLSCLTPASA 191
LLSCLTPASA
Sbjct: 181 LLSCLTPASA 191

□ >gi|1765881|dbj|BAA13622.1| core, env and part of E2/NS1 [Hepatitis C virus]
Length = 414

Score = 280 bits (716), Expect = 1e-74
Identities = 141/191 (73%), Positives = 142/191 (74%)

Query: 1 MSTLPKPQXXXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MSTLPKPQ P DVKFPGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTLPKPQRKTKRNTNRRPMDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNECGWAGWLSPRGSRPHGPNDPRRRSRN LG 120
RRQPIPKAR QGRHWAQPGYPWPLYGNECGWAGWL+SPRGSRPHGPNDP RSRNLG
Sbjct: 61 RRQPIPKARPSQGRHWAQPGYPWPLYGNECGWAGWLSPRGSRPHGPNDPRHRSRN LG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI R IEDGINYATGNLPGCSFSIF LA
Sbjct: 121 KVIDTLCGFADLMGYIPVVGAPLGGVAAALAHGVRVIEDGINYATGNLPGCSFSIFFLA 180

Query: 181 LLSCLTPASA 191
LLSCLTPASA
Sbjct: 181 LLSCLTPASA 191

□ >gi|7650248|gb|AAF65955.1| polyprotein [Hepatitis C virus]
Length = 3010

Score = 280 bits (715), Expect = 1e-74
Identities = 137/191 (71%), Positives = 141/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MST PKPQ P DVKFPGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRAKTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP+WGP DPRRRRSRNLG
Sbjct: 61 RRQPIPKARQPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPNWGPTDPRRRRSRNLG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLTTPASA
Sbjct: 181 LLSCLTTPASA 191

>gi|464178|dbj|BAA03581.1| polyprotein [Hepatitis C virus]
Length = 3011

Score = 279 bits (714), Expect = 2e-74
Identities = 136/191 (71%), Positives = 141/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MST PKPQ P DVKFPGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRAKTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKAR+P+GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRP WGP+DPRRRRSRNLG
Sbjct: 61 RRQPIPKARRPEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPSPDPRRRRSRNLG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTVPASA 191

>gi|1765885|dbj|BAA13624.1| core, env and part of E2/NS1 [Hepatitis C virus]
Length = 414

Score = 279 bits (714), Expect = 2e-74
Identities = 142/191 (74%), Positives = 145/191 (75%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MSTLPKPQ P DVKFPGG+IV ATRKTTSERSQPRG
Sbjct: 1 MSTLPKPQRKTKRNTYRRPMDVKFPGGKIVGGVYLLPRRGPRLGVRAKTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKARQ QGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG
Sbjct: 61 RRQPIPKARQSQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI RA+EDGIN+ATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLMGYIPVVGAPLGGVAAFAHGVRALEDGINFATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLTTPASA
Sbjct: 181 LLSCLTTPASA 191

>gi|1765879|dbj|BAA13621.1| core, env and part of E2/NS1 [Hepatitis C virus]
Length = 414

Score = 279 bits (713), Expect = 2e-74
Identities = 142/191 (74%), Positives = 144/191 (75%)

Query: 1 MSTLPKPQXXXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXATRKTSERSQPRG 60
MSTLPKPQO P DVKFPGGGQIV ATRKTSERSQPRG
Sbjct: 1 MSTLPKPQRKTKRNTNRRPMDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKARQP GRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRP+WGPNPDRRSRNLG
Sbjct: 61 RRQPIPKARQPTGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRNWGPNPDRRSRNLG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDT+TCG ADLMGYI RAIEDGINYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTITCGVADLMGYIPVLGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLTTPASA
Sbjct: 181 LLSCLTTPASA 191

>gi|1765887|dbj|BAA13625.1| core, env and part of E2/NS1 [Hepatitis C virus]
Length = 414

Score = 279 bits (713), Expect = 3e-74
Identities = 142/191 (74%), Positives = 144/191 (75%)

Query: 1 MSTLPKPQXXXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXATRKTSERSQPRG 60
MSTLPKPQO P D+KFPGGQIV ATRKTSERSQPRG
Sbjct: 1 MSTLPKPQRKTKRNTNRRPMDIKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKARQ QGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPDRRSRNLG
Sbjct: 61 RRQPIPKARQSQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPDRRSRNLG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI RA+EDGINYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLMGYIPVVGAPLGGVAAFAHGVRALEDGINYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLTTP SA
Sbjct: 181 LLSCLTTPASA 191

>gi|7650256|gb|AAF65959.1| polyprotein [Hepatitis C virus]
Length = 3010

Score = 278 bits (712), Expect = 3e-74

Identities = 137/191 (71%), Positives = 141/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPKLGVRA TRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGP+DPRRRSRNLG
Sbjct: 61 RRQPIPKARQPEGRSWAQPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI RA+EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLMGYIPLVGAPLGGVARALAHGVRAVEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTIPASA 191

>gi|482138|pir||S40770 genome polyprotein - hepatitis C virus
gi|221587|dbj|BAA01582.1| polyprotein precursor [Hepatitis C virus]
Length = 3011

Score = 278 bits (712), Expect = 4e-74
Identities = 135/191 (70%), Positives = 140/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MST+PKPQ P DVKFPGGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTIPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
RRQPIPK R+P+GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61 RRQPIPKVRRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTVPASA 191

>gi|2327073|gb|AAB67037.1| polyprotein [Hepatitis C virus strain H77]
Length = 3011

Score = 278 bits (711), Expect = 4e-74
Identities = 136/191 (71%), Positives = 140/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
RRQPIPKAR+P+GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLMGYIPLVGAPLGGALARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTPASA 191

>gi|471117|dbj|BAA01728.1| polyprotein precursor [Hepatitis C virus]
Length = 3010

Score = 278 bits (711), Expect = 4e-74
Identities = 137/191 (71%), Positives = 141/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
RRQPIPKAR+P+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGPNDPRRRSRN LG
Sbjct: 61 RRQPIPKARRPEGRAWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRN LG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI RA+EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLMGYIPLVGAPLGGALARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTPASA 191

>gi|130461|sp|P27958|POLG_HCVH Genome polyprotein [Contains: Capsid protein C (C (P22); Envelope glycoprotein E1 (GP32) (GP35); Envelope glycoprotein E2 (GP68) (GP70) (NS1); Protein P7; Nonstructural protein NS2 (P21) ; Protease/helicase NS3 (P70) (Hepacivirin) ; Nonstructural protein NS4A (P4); Nonstructural protein NS4B (P27); Nonstructural protein NS5A (P56); Nonstructural protein NS5B (P66) (P70) (RNA-directed RNA polymerase)]
gi|74464|pir||GNWVCH genome polyprotein - hepatitis C virus (strain H)
gi|329738|gb|AAA45534.1| polyprotein
Length = 3011

Score = 278 bits (711), Expect = 4e-74
Identities = 136/191 (71%), Positives = 140/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
RRQPIPKAR+P+GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRP WGP DPRRRSRN LG
Sbjct: 61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRN LG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA

Subjct: 121 KVIDTLCGFADLMGYIPLVGAPLGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191

LLSCLT PASA

Subjct: 181 LLSCLTVPASA 191

>gi|8926245|gb|AAF81759.1| polyprotein [Hepatitis C virus]

Length = 3011

Score = 278 bits (711), Expect = 4e-74

Identities = 136/191 (71%), Positives = 140/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXXXPTDVKFPGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MST PKPQ P DVKFPGGQIV ATRKTTSERSQPRG

Subjct: 1 MSTNPKPQKRKTRNNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
RRQPIPKAR+P+GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG

Subjct: 61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRN LG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA

Subjct: 121 KVIDTLCGFADLMGYIPLVGAPLGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191

LLSCLT PASA

Subjct: 181 LLSCLTVPASA 191

>gi|130455|sp|P26664|POLG_HCV1 Genome polyprotein [Contains: Capsid protein C (C

(P22); Envelope glycoprotein E1 (GP32) (GP35); Envelope

glycoprotein E2 (GP68) (GP70) (NS1); Protein P7;

Nonstructural protein NS2 (P21); Protease/helicase NS3

(P70) (Hepacivirin); Nonstructural protein NS4A (P4);

Nonstructural protein NS4B (P27); Nonstructural protein

NS5A (P56); Nonstructural protein NS5B (P66) (P70)

(RNA-directed RNA polymerase)]

gi|74463|pir|GNWVC3 genome polyprotein - hepatitis C virus (strain HCV-1)

gi|329874|gb|AAA45676.1| HCV-1

Length = 3011

Score = 278 bits (711), Expect = 4e-74

Identities = 136/191 (71%), Positives = 140/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXXXPTDVKFPGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MST PKPQ P DVKFPGGQIV ATRKTTSERSQPRG

Subjct: 1 MSTNPKPQKKNRNNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
RRQPIPKAR+P+GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG

Subjct: 61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRN LG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA

Subjct: 121 KVIDTLCGFADLMGYIPLVGAPLGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTPASA 191

LLSCLT PASA

Sbjct: 181 LLSCLTVPASA 191

□>gi|14532245|gb|AAK66554.1| HCV type 1a/1b chimera polyprotein [synthetic construct]
gi|14532247|gb|AAK66555.1| HCV type 1a polyprotein [synthetic construct]
gi|14532249|gb|AAK66556.1| HCV type 1a/1b chimera polyprotein [synthetic construct]
Length = 3011

Score = 278 bits (710), Expect = 5e-74

Identities = 136/191 (71%), Positives = 140/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXATRKTSERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTSERSQPRG

Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
RRQPIPKAR+P+GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRP WGP DPRRRSRNLG

Sbjct: 61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA

Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGALARAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTPASA 191

LLSCLT PASA

Sbjct: 181 LLSCLTVPASA 191

□>gi|2327071|gb|AAB67036.1| polyprotein [Hepatitis C virus strain H77]
Length = 3011

Score = 278 bits (710), Expect = 5e-74

Identities = 136/191 (71%), Positives = 140/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXATRKTSERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTSERSQPRG

Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
RRQPIPKAR+P+GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRP WGP DPRRRSRNLG

Sbjct: 61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA

Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGALARAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTPASA 191

LLSCLT PASA

Sbjct: 181 LLSCLTVPASA 191

□>gi|22129793|ref|NP_671491.1| polyprotein [Hepatitis C virus]
gi|2316098|gb|AAB66324.1| polyprotein [Hepatitis C virus]

Length = 3011

Score = 278 bits (710), Expect = 5e-74
Identities = 136/191 (71%), Positives = 140/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXATRKTSESRQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTSESRQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRG 60

Query: 61 RRQPIPCKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
RRQPIPCKAR+P+GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61 RRQPIPCKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTVVPASA 191

>gi|14532251|gb|AAK66557.1| HCV type 1a/1b chimera mutant polyprotein [synthetic
Length = 3011

Score = 278 bits (710), Expect = 5e-74
Identities = 136/191 (71%), Positives = 140/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXATRKTSESRQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTSESRQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRG 60

Query: 61 RRQPIPCKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
RRQPIPCKAR+P+GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61 RRQPIPCKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTVVPASA 191

>gi|2327075|gb|AAB67038.1| polyprotein [Hepatitis C virus strain H77]
Length = 3011

Score = 278 bits (710), Expect = 5e-74
Identities = 136/191 (71%), Positives = 140/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXATRKTSESRQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTSESRQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRG 60

Query: 61 RRQPIPCKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
RRQPIPCKAR+P+GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61 RRQPIPCKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGALARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTVPASA 191

>gi|9930557|gb|AAG02099.1| polyprotein [Hepatitis C virus]
Length = 3011

Score = 278 bits (710), Expect = 5e-74
Identities = 136/191 (71%), Positives = 140/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKAR+P+GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRP WGP DPRRRRSRNLG
Sbjct: 61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGALARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTVPASA 191

>gi|3098655|gb|AAC15732.1| polyprotein [Hepatitis C virus]
Length = 2864

Score = 277 bits (709), Expect = 6e-74
Identities = 136/191 (71%), Positives = 139/191 (72%)

Query: 1 MSTLPKPQXXXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGP DPRRRRSRNLG
Sbjct: 61 RRQPIPKARQPEGRAWAQPGYPWPLYGNEGGLGAGWLLSPRGSRPSWGPTDPRRRRSRNLG 120

Query: 121 KVIDTLTCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLTCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLTCGFADLMGYIPLVGAPLGGALARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTIPASA 191

>gi|15529111|gb|AAK97744.1| polyprotein [Hepatitis C virus]
Length = 3010

Score = 277 bits (709), Expect = 6e-74
Identities = 136/191 (71%), Positives = 139/191 (72%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MST PKPQ P DVKFPGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRSRNLG 120
RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61 RRQPIPKARQPEGRAWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLMGYIPLVGAPLGGVARALAHGVRVVEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTTIPASA 191

>gi|1944376|dbj|BAA19625.1| unnamed protein product [Hepatitis C virus]
Length = 3010

Score = 277 bits (709), Expect = 7e-74
Identities = 136/191 (71%), Positives = 141/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MST PKPQ P DVKFPGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRSRNLG 120
RRQPIPKAR+P+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP+WGP DPRRRSRNLG
Sbjct: 61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPNWGPTDPRRRSRNLG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTTPASA 191
LLSCLTTTPASA
Sbjct: 181 LLSCLTTTPASA 191

>gi|1009261|dbj|BAA07091.1| core, env and part of E2/NS1 [Hepatitis C virus]
Length = 414

Score = 277 bits (709), Expect = 7e-74
Identities = 142/191 (74%), Positives = 142/191 (74%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MSTLPKPQ P DVKFPGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTLPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRSRNLG 120

RRQPIPKAR GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRSRNLG
Sbjct: 61 RRQPIPKARHQTGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRSRNLG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI RAIEDGINYATGNLPGCSFSIFLLA

Sbjct: 121 KVIDTLCGFADLMGYI PVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLTTPASA

Sbjct: 181 LLSCLTTPASA 191

>gi|3098644|gb|AAC15727.1| polyprotein [Hepatitis C virus]
Length = 2864

Score = 277 bits (709), Expect = 7e-74
Identities = 136/191 (71%), Positives = 139/191 (72%)

Query: 1 MSTLPKPQXXXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRSRNLG 120
RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGP DPRRSRNLG
Sbjct: 61 RRQPIPKARQPEGRAWAQPGYPWPLYGNEGGLWAGWLLSPRGSRPSWGPDTDPRRSRNLG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLT PASA

Sbjct: 181 LLSCLTIPASA 191

>gi|5918961|gb|AAD56196.1| polyprotein [Hepatitis C virus]
Length = 3010

Score = 277 bits (709), Expect = 8e-74
Identities = 136/191 (71%), Positives = 141/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRSRNLG 120
RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGP+DPRRSRNLG
Sbjct: 61 RRQPIPKARQPEGRTWAQPGYPWPLYGNEGGMWAGWLLSPRGSRPSWGPSPDPRRSRNLG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADL+GYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLLGYIPLVGAPIGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLTTPASA

Sbjct: 181 LLSCLTTPASA 191

□ >gi|2943784|gb|BAA25076.1| polyprotein [Hepatitis C virus]
Length = 3010

Score = 277 bits (708), Expect = 8e-74
Identities = 136/191 (71%), Positives = 140/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKAR+P+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGPNDPRRRSRNLG
Sbjct: 61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGGLGWAGWLLSPRGSRPSWGPNDPRRRSRNLG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTIPASA 191

□ >gi|7650246|gb|AAF65954.1| polyprotein [Hepatitis C virus]
Length = 3010

Score = 277 bits (708), Expect = 8e-74
Identities = 136/191 (71%), Positives = 139/191 (72%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61 RRQPIPKARQPEGRAWAQPGYPWPLYGNEGGLGWAGWLLSPRGSRPSWGPNDPRRRSRNLG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTIPASA 191

□ >gi|7650240|gb|AAF65951.1| polyprotein [Hepatitis C virus]
Length = 3010

Score = 277 bits (708), Expect = 9e-74
Identities = 136/191 (71%), Positives = 139/191 (72%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNECGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61 RRQPIPKARQPEGRAWAQPGYPWPLYGNEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLMGYIPLVGAPLGGARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTIPASA 191

>gi|5420377|emb|CAB46677.1| polyprotein [Hepatitis C virus type 1b]
Length = 3010

Score = 277 bits (708), Expect = 9e-74
Identities = 136/191 (71%), Positives = 139/191 (72%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MST PKPQ P DVKFPGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTNPKPQKRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNECGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61 RRQPIPKARQPEGRAWAQPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLMGYIPLVGAPLGGARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTIPASA 191

>gi|5918963|gb|AAD56197.1| polyprotein [Hepatitis C virus]
Length = 3010

Score = 277 bits (708), Expect = 9e-74
Identities = 136/191 (71%), Positives = 141/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MST PKPQ P DVKFPGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTNPKPQKRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNECGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGP+DPRRRSRNLG
Sbjct: 61 RRQPIPKARQPEGRTWAQPGYPWPLYGNEGMGWAGWLLSPRGSRPSWGPDPRRRSRNLG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADL+GYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLGYIPLVGAPIGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLTTPASA

Sbjct: 181 LLSCLTPASA 191

□ >gi|7650244|gb|AAF65953.1| polyprotein [Hepatitis C virus]
Length = 3010

Score = 277 bits (708), Expect = 9e-74
Identities = 137/191 (71%), Positives = 140/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXATRKTTSERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGPNDPRRRSRN LG
Sbjct: 61 RRQPIPKARQPEGRAWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRN LG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTPASA 191
LLS LTTPASA
Sbjct: 181 LLSGLTTPASA 191

□ >gi|7650224|gb|AAF65943.1| polyprotein [Hepatitis C virus]
Length = 3010

Score = 277 bits (708), Expect = 1e-73
Identities = 136/191 (71%), Positives = 139/191 (72%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXATRKTTSERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
RRQPIPK RQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGP D PRRRSRN LG
Sbjct: 61 RRQPIPKVRQPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRN LG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLMGYIPLVGAPLGGAAARVLAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTPASA 191
LLSCLTPASA
Sbjct: 181 LLSCLTPASA 191

□ >gi|7650234|gb|AAF65948.1| polyprotein [Hepatitis C virus]
Length = 3010

Score = 277 bits (708), Expect = 1e-73
Identities = 136/191 (71%), Positives = 139/191 (72%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXXATRKTTSERSQPRG 60

MST PKPQ P DVKFPGGQIV ATRKTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61 RRQPIPKARQPEGRAWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLCGFADLGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTVPASA 191

>gi|7341103|gb|AAF61205.1| polyprotein [Hepatitis C virus]
Length = 3008

Score = 276 bits (707), Expect = 1e-73
Identities = 136/191 (71%), Positives = 140/191 (73%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGQIVXXXXXXXXXXXXATRKTSERSQPRG 60
MST PKPQ P DVKFPGGQIV ATRKTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP+WGP DPRRRSRNLG
Sbjct: 61 RRQPIPKARQPEGRAWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPNWGPTDPRRRSRNLG 120

Query: 121 KVIDTLCGFADLGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTIPASA 191

>gi|1814086|dbj|BAA09072.1| polyprotein [Hepatitis C virus]
Length = 3010

Score = 276 bits (707), Expect = 1e-73
Identities = 136/191 (71%), Positives = 139/191 (72%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGQIVXXXXXXXXXXXXATRKTSERSQPRG 60
MST PKPQ P DVKFPGGQIV ATRKTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRN LG 120
RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61 RRQPIPKARQPEGRAWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLCGFADLGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLGYIPLVGAPLGGASRALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTIPASA 191

>gi|7650252|gb|AAF65957.1| polyprotein [Hepatitis C virus]
Length = 3010

Score = 276 bits (707), Expect = 1e-73
Identities = 136/191 (71%), Positives = 139/191 (72%)

Query: 1 MSTLPKPQXXXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLSPRGSRPHWGPNDPRRRSRN LG 120
RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61 RRQPIPKARQPEGRTWAQPGYPWPLYGNEGGMGWAGWLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI R +ED +NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDSVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTPASA 191
LLSCLTPASA
Sbjct: 181 LLSCLTPASA 191

>gi|1814089|gb|BAA09076.1| polyprotein [Hepatitis C virus]
Length = 3010

Score = 276 bits (707), Expect = 1e-73
Identities = 136/191 (71%), Positives = 139/191 (72%)

Query: 1 MSTLPKPQXXXXXXXXXXXXPTDVKFPGGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MST PKPQ P DVKFPGGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLSPRGSRPHWGPNDPRRRSRN LG 120
RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLSPRGSRP WGP DPRRRSRNLG
Sbjct: 61 RRQPIPKARQPEGRAWAQPGYPWPLYGNEGGMGWAGWLSPRGSRPSWGPTDPRRRSRNLG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLMGYIPLVGAPLGGASRALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTPASA 191
LLSCLT PASA
Sbjct: 181 LLSCLTIPASA 191

>gi|1765868|gb|BAA13615.1| core, env and part of E2/NS1 [Hepatitis C virus]
Length = 414

Score = 276 bits (706), Expect = 1e-73
Identities = 140/191 (73%), Positives = 142/191 (74%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MSTLPKPQ P DVKFPGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTLPKPQRKTKRNTNRRPMDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKARQP GR W QPGYPWPLYGNEGCGWAGWLLSPRGSRP+WGPNDPRRRSRNLG
Sbjct: 61 RRQPIPKARQPTGRSGQPGYPWPLYGNEGCGWAGWLLSPRGSRPNWGPNDPRRRSRNLG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCG ADLMGYI RAIEDG+NYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGLADLMGYIPVLLGGPLGGVAAALAHGVRAIEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLTTPASA
Sbjct: 181 LLSCLTTPASA 191

>gi|1009263|gb|BAA07092.1| core, env and part of E2/NS1 [Hepatitis C virus]
Length = 414

Score = 276 bits (706), Expect = 1e-73
Identities = 141/191 (73%), Positives = 142/191 (74%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MSTLPKPQ P DVKFPGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTLPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKAR GR WAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG
Sbjct: 61 RRQPIPKARHQTGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI RA+EDGINYATGNLPGCSFSIFLLA
Sbjct: 121 KVIDTLCGFADLMGYIPVVGAPLGGVAAALAHGVRALEDGINYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191
LLSCLTTPASA
Sbjct: 181 LLSCLTTPASA 191

>gi|7650226|gb|AAF65944.1| polyprotein [Hepatitis C virus]
Length = 3010

Score = 276 bits (706), Expect = 2e-73
Identities = 136/191 (71%), Positives = 139/191 (72%)

Query: 1 MSTLPKPQXXXXXXXXXXPTDVKFPGGQIVXXXXXXXXXXXXATRKTTSERSQPRG 60
MST PKPQ P DVKFPGGQIV ATRKTTSERSQPRG
Sbjct: 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTTSERSQPRG 60

Query: 61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
RRQPIPKARQP+GR WAQPGYPWPLYGNEG GWAGWLLSPRGSRP WGP DPRRRRSRNLG
Sbjct: 61 RRQPIPKARQPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPDTDPRRRSRNLG 120

Query: 121 KVIDTLCGFADLMGYIXXXXXXXXXXXXXXXXXRAIEDGINYATGNLPGCSFSIFLLA 180
KVIDTLCGFADLMGYI R +EDG+NYATGNLPGCSFSIFLLA

Sbjct: 121 KVIDTLTCGFADLIMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180

Query: 181 LLSCLTTPASA 191

LLSCLT PASA

Sbjct: 181 LLSCLTIPASA 191

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF excluding environmental samples

Posted date: May 11, 2004 12:59 AM

Number of letters in database: 593,787,773

Number of sequences in database: 1,798,171

Lambda K H
0.320 0.140 0.471

Gapped

Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 42,029,332

Number of Sequences: 1798171

Number of extensions: 1637745

Number of successful extensions: 3615

Number of sequences better than 10.0: 298

Number of HSP's better than 10.0 without gapping: 294

Number of HSP's successfully gapped in prelim test: 4

Number of HSP's that attempted gapping in prelim test: 3029

Number of HSP's gapped (non-prelim): 302

length of query: 191

length of database: 593,787,773

effective HSP length: 118

effective length of query: 73

effective length of database: 381,603,595

effective search space: 27857062435

effective search space used: 27857062435

T: 11

A: 40

X1: 16 (7.4 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.7 bits)

S2: 70 (31.6 bits)